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Supplementary material

Table S1. Characteristics of the *Senecio pterophorus* populations used in this study and summary of genetic diversity metrics estimated as the percentage of polymorphic loci, *PLP*, the average gene diversity, *H*j, and band richness after rarefaction *B*r(5). Populations are classified in sub-regional groups in the South African native range, Australia and Spain. n = number of individuals, NL= number of polymorphic AFLP loci.

Region/ Group[1]	Population name	Pop. Code	Origin[2]	Coordinates	Herbarium code	n	NL	*PLP (%)*	*H*j (mean ± SE)	*B*r(5)
SOUTH AFRICA										
SA-1	Colchester	S06	N	33º41'S 25º49'E	BCN 78089	8	176	53.8	0.193 ± 0.010	1.342
SA-1	Grahamstown	S07	N	33º19'S 26º32'E	BCN 78090	9	190	58.1	0.191 ± 0.010	1.355
SA-1	Alexandria	S08	N	33º36'S 26º24'E	BCN 78091	9	231	70.6	0.237 ± 0.010	1.466
SA-1	Port Alfred	S09	N	33º36'S 26º52'E	BCN 78092	9	217	66.4	0.219 ± 0.010	1.409
SA-1	Stafford's Post	S16	N	30º31'S 29º46'E	BCN 78101	4	169	51.7	0.210 ± 0.010	——
SA-2	Franklin	S17	N	30º23'S 29º38'E	BCN 78110	4	187	57.2	0.256 ± 0.011	——
SA-2	Sidwadwenii	S20	N	31º24'S 28º50'E	——	6	194	59.3	0.232 ± 0.011	1.407
SA-2	Mqanduli	S21	N	31º50'S 28º46'E	——	4	188	57.5	0.258 ± 0.011	——
SA-2	Gwadana	S22	N	32º13'S 28º17'E	——	6	180	55.0	0.207 ± 0.010	1.374
SA-2	Nobokwe	S23	N	31º55'S 27º50'E	——	6	182	55.7	0.205 ± 0.010	1.361
SA-3	Fort Hare	S10	N	32º47'S 26º52'E	BCN 78093	9	243	74.3	0.253 ± 0.010	1.485
SA-3	Courtlands	S11	N	32º40'S 28º00'E	BCN 78094	4	208	63.6	0.284 ± 0.010	——
SA-3	Umtentu	S12	N	31º51'S 28º30'E	BCN 78095	5	207	63.3	0.257 ± 0.010	1.480
SA-3	Flagstaff	S13	N	31º11'S 29º26'E	BCN 78096	10	210	64.2	0.220 ± 0.010	1.408
SA-3	Mt. Alyliff	S14	N	30º50'S 29º15'E	BCN 78097	4	168	51.4	0.220 ± 0.011	——
SA-3	Bizana	S15	N	30º50'S 29º35'E	BCN 78098	4	188	57.5	0.240 ± 0.010	——
SA-3	Mount Frere	S18	N	30º57'S 28º57'E	BCN 78114	9	192	58.7	0.191 ± 0.010	1.341
SA-3	Antioch	S19	N	30º42'S 28º51'E	BCN 78116	7	188	57.5	0.211 ± 0.010	1.359
W. CAPE	Groenfonteinkop	S01	E	33º47'S 18º52'E	BCN 78080	9	166	50.8	0.163 ± 0.010	1.259
W. CAPE	Cape Town	S02	E	34º07'S 18º23'E	BCN 78082	6	169	51.7	0.174 ± 0.010	1.275
W. CAPE	Elgin	S03	E	34º09'S 19º01'E	BCN 78083	5	203	62.1	0.244 ± 0.010	1.413
W. CAPE	Hermanus	S04	E	34º24'S 19º11'E	BCN 78085	6	196	59.9	0.212 ± 0.010	1.350
W. CAPE	Cape Town	S05	E	33º56'S 18º26'E	BCN 78086	7	220	67.3	0.244 ± 0.010	1.474
AUSTRALIA										
A-SYD	Doonside	A01	I	33º45'S 150º52'E	BCN 111744	6	158	48.3	0.181 ± 0.010	1.292
A-SYD	Newcastle	A02	I	32º52'S 151º41'E	BCN 111743	9	178	54.4	0.168 ± 0.010	1.267
A-EYRE	Port Lincoln	A03	I	34º33'S 135º49'E	BCN 111742	9	191	58.4	0.199 ± 0.010	1.361
A-EYRE	Wangary	A04	I	34º30'S 135º25'E	BCN 111741	10	201	61.5	0.194 ± 0.010	1.346
A-EYRE	Lincoln NP	A05	I	34º48'S 135º46'E	BCN 111740	10	194	59.3	0.120 ± 0.010	1.360
A-EYRE	Hincks NP	A06	I	33º55'S 136º14'E	BCN 111753	7	158	48.3	0.178 ± 0.011	1.290
A-ADE	Mt. Compass	A07	I	35º20'S 138º36'E	BCN 111752	6	179	54.7	0.209 ± 0.011	1.376
A-ADE	Cleland NP	A08	I	34º57'S 138º42'E	BCN 111750	6	182	55.7	0.218 ± 0.011	1.358
A-ADE	Warren CP	A09	I	34º40'S 138º51'E	BCN 111749	5	173	52.9	0.206 ± 0.010	1.343

Region/ Group[1]	Population name	Pop. Code	Origin[2]	Coordinates	Herbarium code	n	NL	*PLP (%)*	*Hj* (mean ± SE)	*Br*(5)
A-BM	Mt. Burr	A10	I	37º35'S 140º28'E	BCN 111748	4	205	62.7	0.269 ± 0.010	—
A-BM	Mt. Napier NP	A11	I	37º55'S 142º02'E	BCN 111747	8	220	67.3	0.232 ± 0.010	1.443
A-MEL	Hastings	A12	I	38º17'S 145º11'E	BCN 111746	9	177	54.1	0.140 ± 0.009	1.228
A-MEL	Gumbaya Park	A13	I	38º04'S 145º39'E	BCN 111745	2	142	43.4	0.116 ± 0.008	—
EUROPE										
Spain										
CAT-S	Cambrils	C01	I	41º04'N 1º04'E	BCN 111771	8	174	53.2	0.177 ± 0.010	1.289
CAT-N	Palafolls	C02	I	41º39'N 2º42'E	BCN 111770	9	202	61.8	0.207 ± 0.010	1.364
CAT-N	Calella	C03	I	41º37'N 2º39'E	BCN 111769	8	199	60.9	0.210 ± 0.010	1.357
CAT-N	Castellbisbal	C04	I	41º27'N 1º59'E	BCN 111768	6	183	56.0	0.211 ± 0.010	1.349
CAT-N	Castellar V.	C05	I	41º36'N 2º04'E	BCN 111767	5	150	45.9	0.161 ± 0.010	1.251
CAT-N	Bigues i Riells	C06	I	41º41'N 2º12'E	BCN 111766	2	158	48.3	0.170 ± 0.010	—
CAT-N	Sabadell	C07	I	41º31'N 2º07'E	BCN 111765	4	192	58.7	0.254 ± 0.010	—
CAT-N	Ripollet	C08	I	41º29'N 2º10'E	BCN 111764	6	158	48.3	0.162 ± 0.009	1.260
CAT-N	Matadepera	C09	I	41º35'N 2º01'E	BCN 111763	6	206	63.0	0.249 ± 0.011	1.415
CAT-N	Sant Llorenç NP	C10	I	41º36'N 2º05'E	BCN 111757	7	197	60.2	0.223 ± 0.010	1.394
CAT-N	Campins	C11	I	41º43'N 2º28'E	BCN 111756	4	174	53.2	0.237 ± 0.011	—
CAT-N	Montseny NP	C12	I	41º43'N 2º24'E	BCN 111755	3	146	44.6	0.206 ± 0.010	—
CAT-N	Viladecans	C13	I	41º17'N 2º02'E	—	8	178	54.4	0.181 ± 0.010	1.308
Italy										
ITA	Pietra Ligure	I01	I	44º08'N 8º16'E	BCN 111762	8	223	68.2	0.245 ± 0.010	1.440
ITA	Zucarello	I02	I	44º06'N 8º07'E	BCN 111761	9	209	63.9	0.236 ± 0.011	1.391
ITA	Pontedassio	I03	I	43º56'N 8º00'E	BCN 111760	8	203	62.1	0.236 ± 0.011	1.392
ITA	Arma di Taggia	I04	I	43º50'N 7º51'E	—	10	222	67.9	0.249 ± 0.011	1.454
ITA	Ventimiglia	I05	I	43º49'N 7º35'E	BCN 111759	8	205	62.7	0.239 ± 0.010	1.425
ITA	Vado Ligure	I06	I	44º16'N 8º25'E	BCN 111758	2	151	46.2	0.210 ± 0.010	—

[1] Abbreviation for sub-regional groups. In the South African native range: subgroups SA-1, SA-2 and SA-3 corresponding to lineages following a STRUCTURE analyses (see Fig. 4A). Populations were assigned to each sub-group based on the most frequent lineage. In Australia: A-SYD = Sydney area, A-EYRE = Eyre Peninsula, A-ADE = Adelaide area, A-BM = Barker-Mallee area, A-MEL = Melbourne area; In Spain: CAT-S = South Catalonia, CAT- N= North Catalonia.

[2] Origin: N = native, E = expanded, I = introduced.

Table S2. Primer descriptions, amplification conditions used in this study and GenBank accessions. °C, annealing temperature.

Regions	Primers	**Sequences 5' → 3'**	References[1]	º C	Genbank acc.
ndhC- trnV^{UAC}	ndhC	TAT TAT TAG AAA TGY CCA RAA AAT ATC ATA TTC	[1]	56	KU682190
	trnV$^{(UAC)}$x2	GTC TAC GGT TCG ART CCG TA			
rpL32–trnL^{UAG}	rpL32F	CAG TTC CAA AA A AAC GTA CTT C	[1]	52	KU641238
	trnL$^{(UAG)}$	CTG CTT CCT AAG AGC AGC GT			
trnL–trnF	trnL–e	GGT TCA AGT CCC TCT ATC CC	[2]	58	KU682189
	trnL–f	ATT TGA ACT GGT GCA ACG AG			
trnT–trnLb	trnTA2	CAA ATG CGA TGC TCT AAC CT	[3]	52	KU682191
	trnLb	TCT ACC GAT TTC GCC ATA TC			
rpl16	Rex2	GAT ATT CCC TTC ATT CTT CCT	[4,5]	52	KU605607
	rpl16F71	GCT ATG CTT AGT GTG TGA CTC GTT G			
trnG	3'–trnG^{UUC}	GTA GCG GGA ATC GAA CCC GCA TC	[6]	52	KU641239
	5'–trnG2G	GCG GGT ATA GTT TAG TGG TAA AA			
5'trnK	trnK–3914F	TGG GTT GCT AAC TCA ATG G	[7]	52	KU605608
	matK–1168R	ATT GAA TGA ATT GAT CGT A			
trnL	trnL–c	CGA AAT CGG TAG ACG CTA CG	[2]	58	KU641240
	trnL–d	GGG GAT AGA GGG ACT TGA AC			

[1]References:

[1] Shaw J, Lickey EB, Schilling EE, Small RL (2007) Comparison of whole chloroplast genome sequences to choose noncoding regions for phylogenetic studies in angiosperms: the tortoise and the hare III. Am J Bot 94:275–288

[2] Taberlet P, Gielly L, Pautou G, Bouvet J (1991) Universal primers for amplification of three non–coding regions of chloroplast DNA. Plant Mol Biol 17:1105–1109

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[4] Sanz M, Schönswetter P, Vallès J, Schneeweiss GM, Vilatersana R (2014) Southern isolation and northern long-distance dispersal shaped the phylogeography of the widespread, but highly disjunct, European high mountain plant *Artemisia eriantha* (Asteraceae). Bot J Linn Soc 174:214–226

[5] Jordan WC, Courtney MW, Neigel JE (1996) Low levels of infraspecific genetic variation at a rapidly evolving chloroplast DNA locus in North American duckweeds (Lemnaceae). Am J Bot 83:430–439

[6] Shaw J, Lickey EB, Beck JT, Farmer SB, Liu W, Miller J, Siripun KC, Winder CT, Schilling EE, Small RL (2005) The tortoise and the hare II: relative utility of 21 noncoding chloroplast DNA sequences for phylogenetic analysis. Am J Bot 92:142–166

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Table S3. Summary of the double scoring and error scoring rate. The percentages were calculated in relation to the total number of markers for each primer pair.

Primer combination	Nº samples	Repetitions (%)	Repeatability (%)	Repeatability rang (%)	Error (%)
*Eco*RI–AGG/*Mse*I–CTC	44	12.05	97.00	82.35–100	3.00
*Eco*RI–ACT/*Mse*I–CAA	35	9.59	99.74	97.50–100	0.26
*Eco*RI–AAG/*Mse*I–CAA	33	9.04	97.20	82.61–100	2.80
Mean	37.33	10.22	97.98		2.02

Table S4. Proportion of assignment of Western Cape populations (South Africa expanded populations) and Australian populations to the native South African lineages with minimal log likelihood differences of 0, 1 and 2 based on a test implanted in AFLPOP. South African lineages: SA–1: southern lineage, SA–2: central lineage and SA–3: central/ northern lineage (see Fig. 4A). None = no assignment success

	WESTERN CAPE			AUSTRALIA		
	0	1	2	0	1	2
SA-1	42.4	36.4	33.4	9.0	4.5	3.4
SA-2	3.0	3.0	3.1	20.2	16.9	15.7
SA-3	54.6	51.5	42.4	70.8	57.3	46.1
None	0.0	9.1	21.2	0.0	21.3	34.8

Table S5. Proportion of assignment of populations from the three European colonization events to the native South African lineages and Australian sub-regions with minimal log likelihood differences of 0, 1 and 2 based on a test implanted in AFLPOP. South African lineages: SA–1: southern lineage, SA–2: central lineage and SA–3: central/northern lineage (following STRUCTURE analyses; see Fig. 4A). Australian sub-regions: A-SYD =Sydney populations, A-EYRE = Eyre Peninsula populations, A-ADE = Adelaide populations, A-BM = Barker-Mallee populations, A-MEL = Melbourne populations (see Fig. 1). None = no assignment success

	SPAIN (CAT-S)			SPAIN (CAT-N)			ITALY		
	0	1	2	0	1	2	0	1	2
SA-1	20.0	10.0	10.0	24.6	21.7	14.5	6.7	4.4	4.4
SA-2	0.0	0.0	0.0	11.6	5.8	5.8	4.4	4.4	0.0
SA-3	50.0	50.0	30.0	50.7	43.6	30.4	88.9	82.3	77.8
A-SYD	10.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
A-EYRE	0.0	0.0	0.0	8.7	2.9	2.9	0.0	0.0	0.0
A-ADE	20.0	20.0	20.0	1.5	1.4	0.0	0.0	0.0	0.0
A-BM	0.0	0.0	0.0	2.9	2.9	2.9	0.0	0.0	0.0
A- MEL	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
None	0.0	20.0	40.0	0.0	21.7	43.5	0.0	8.9	17.8

Table S6. Linear models testing differences in the metrics of genetic diversity, *PLP*, *Hj* and *Br*(5), between the native region and each of the non-native regions (Western Cape in South Africa, Australia, Spain and Italy). *PLP* = percentage of polymorphic loci; *Hj* = average gene diversity; *Br*(5) = band richness after rarefaction to 5. Significant results at $p < 0.05$ are indicated in bold.

		Value	*Standard Error*	*t–value*	*p–value*
PLP	Intercept (South Africa native range)	59.767	1.550	38.563	0.000
	Western Cape	–1.407	3.324	–0.423	0.674
	Australia	–4.305	2.393	–1.799	0.078
	Spain	–5.267	2.393	–2.201	0.032
	Italy	2.067	3.100	0.667	0.508
Hj	Intercept (South African native range)	0.2269	0.008	29.279	0.000
	Western Cape	–0.019	0.017	–1.173	0.247
	Australia	–0.040	0.012	–3.340	0.002
	Spain	–0.023	0.012	–1.938	0.058
	Italy	0.009	0.015	0.577	0.566
Br(5)	Intercept (South African native range)	1.402	0.018	78.058	0.000
	Western Cape	–0.048	0.032	–1.499	0.143
	Australia	–0.069	0.025	–2.726	0.009
	Spain	–0.070	0.027	–2.631	0.012
	Italy	0.018	0.032	0.561	0.578

Figure S1. Summary of the AFLP data analyses conducted with the program STRUCTURE. The left graphs show the ΔK for each K value. The right graphs show the mean similarity between runs for each K value. Circles represent the mean of all pairwise comparisons between ten runs and lines indicate the standard deviation. A–B, South African native range. C–D, South African native and expanded range. E–F, South Africa and Australia. G–H, South Africa, Australia and Spain. I–J, South Africa, Australia and Europe (Spain and Italy).

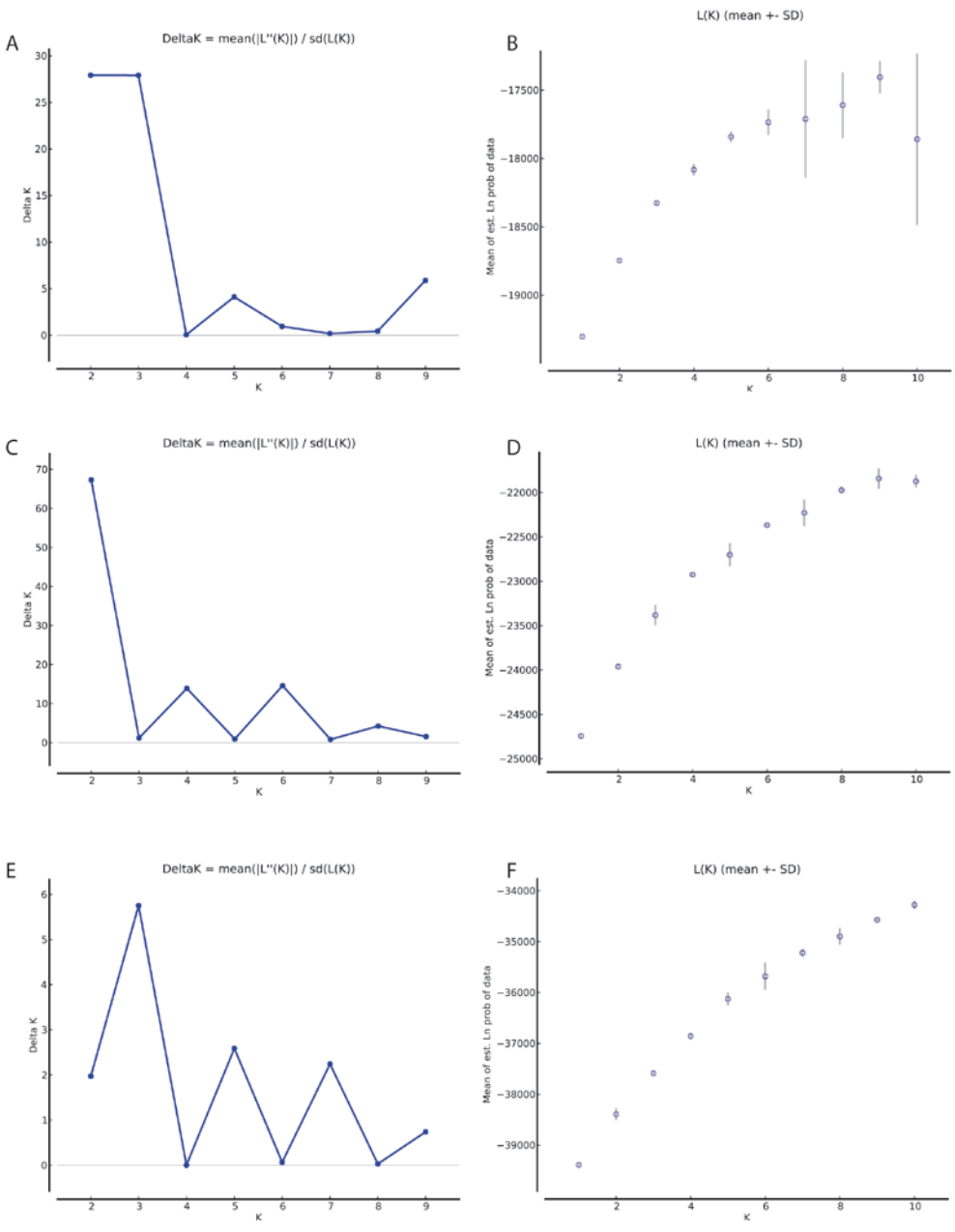


Figure S1 (continued)

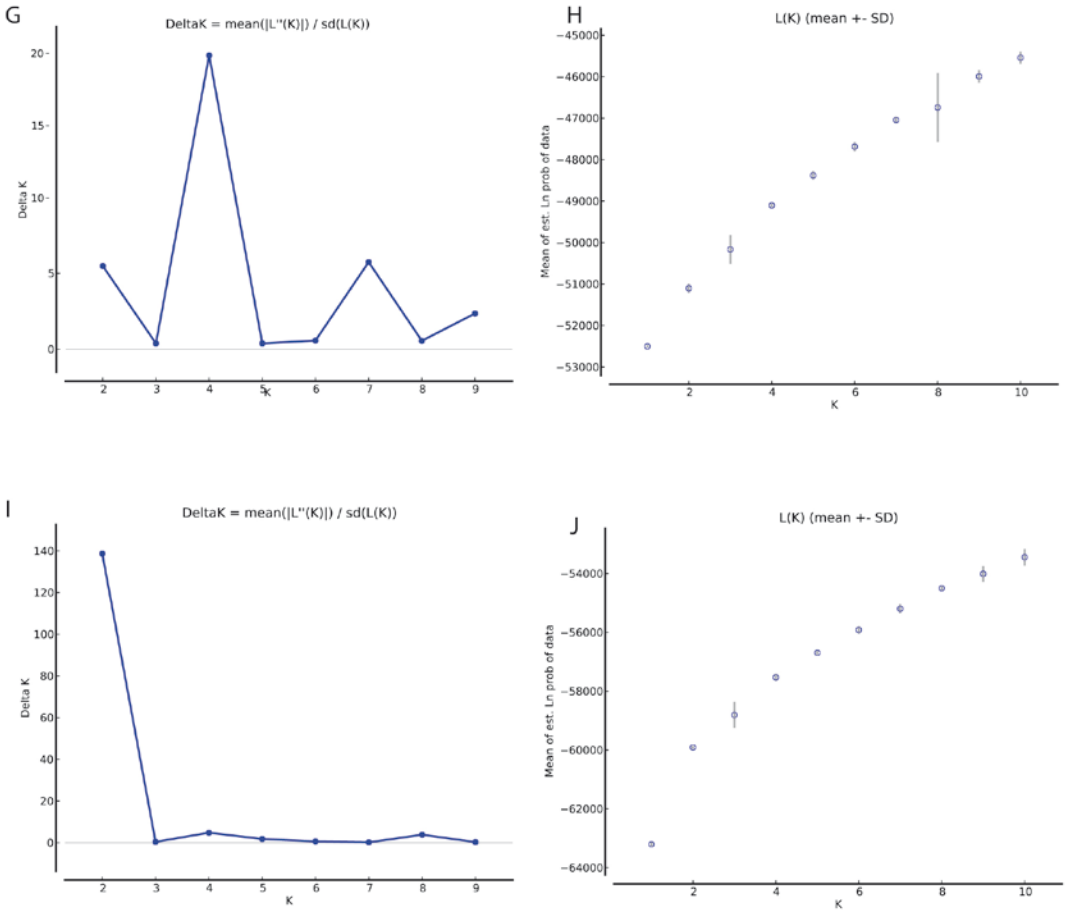
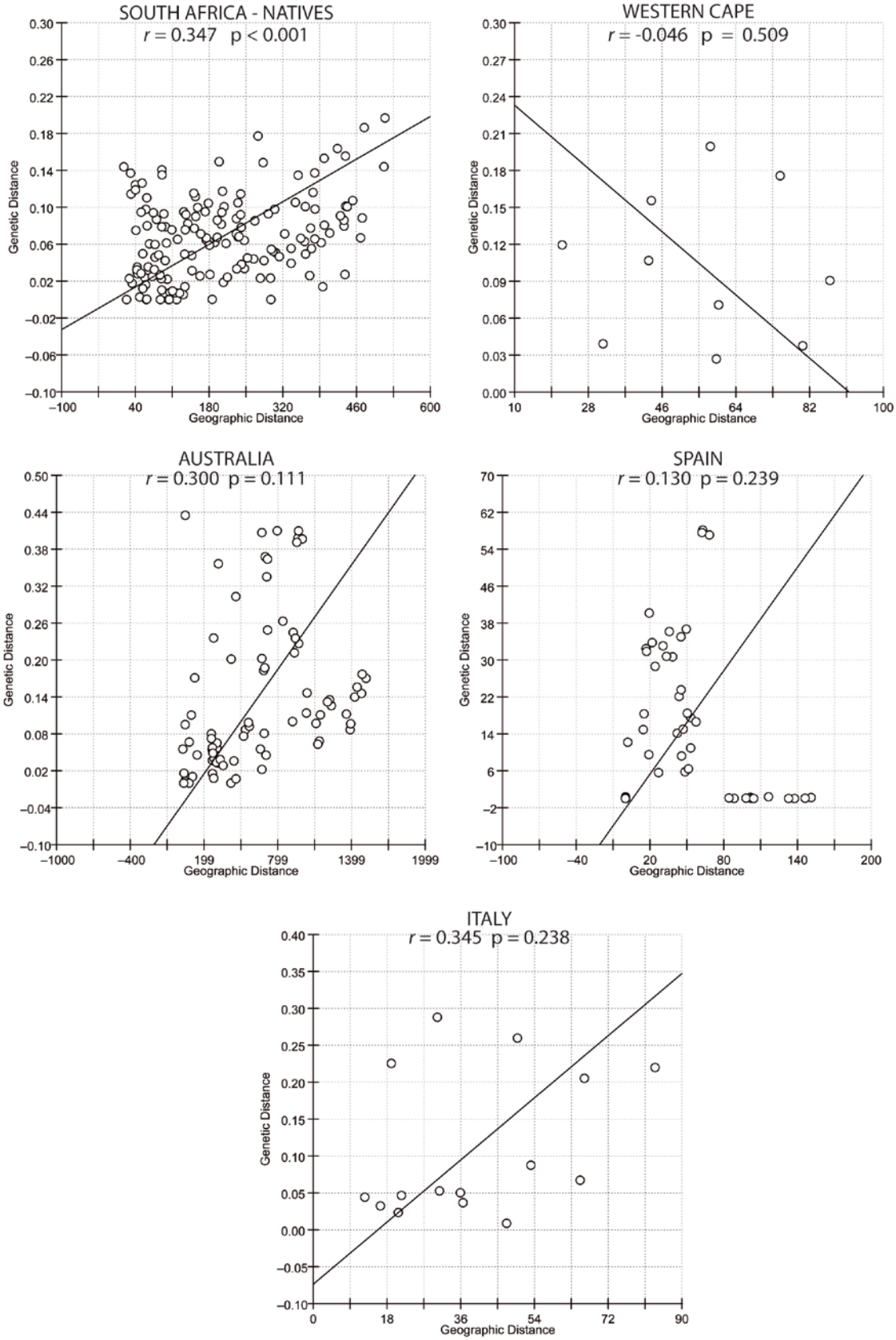


Figure S2. Relationship between genetic distance (F_{ST} values) and geographical distance (km) for population pairs within regions



Vilatersana R, Sanz M, Galian A, Castells E (2016) Biological Invasions
DOI: 10.1007/s10530-016-1150-1

Figure S3. Results of BAPS analysis (*K* = 3) using AFLP markers in native South African samples of *Senecio pterophorus*. Colors identify genetically distinct clusters. South African lineages: SA-1: southern lineage, SA-2: central lineage and SA-3: central/northern lineage.

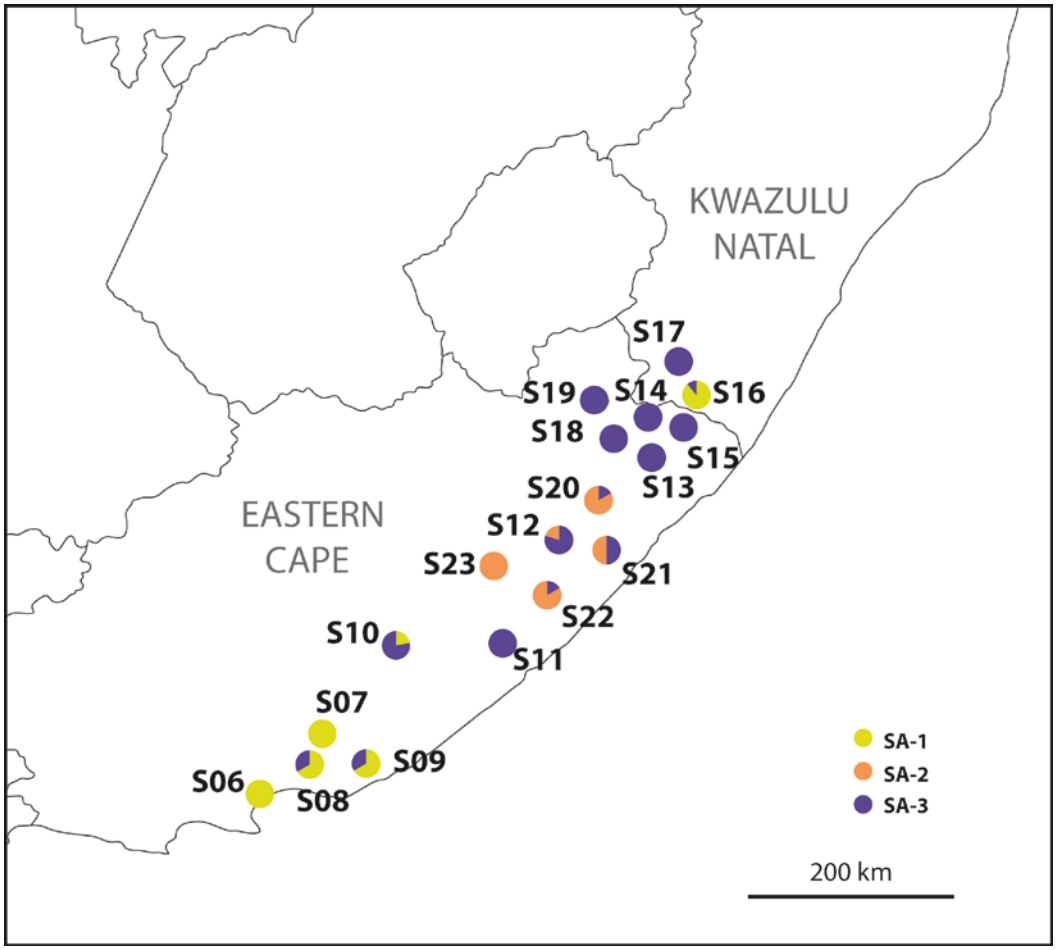


Figure S4. Marker frequency distribution for each of the five ranges studied. Only polymorphic markers are included.

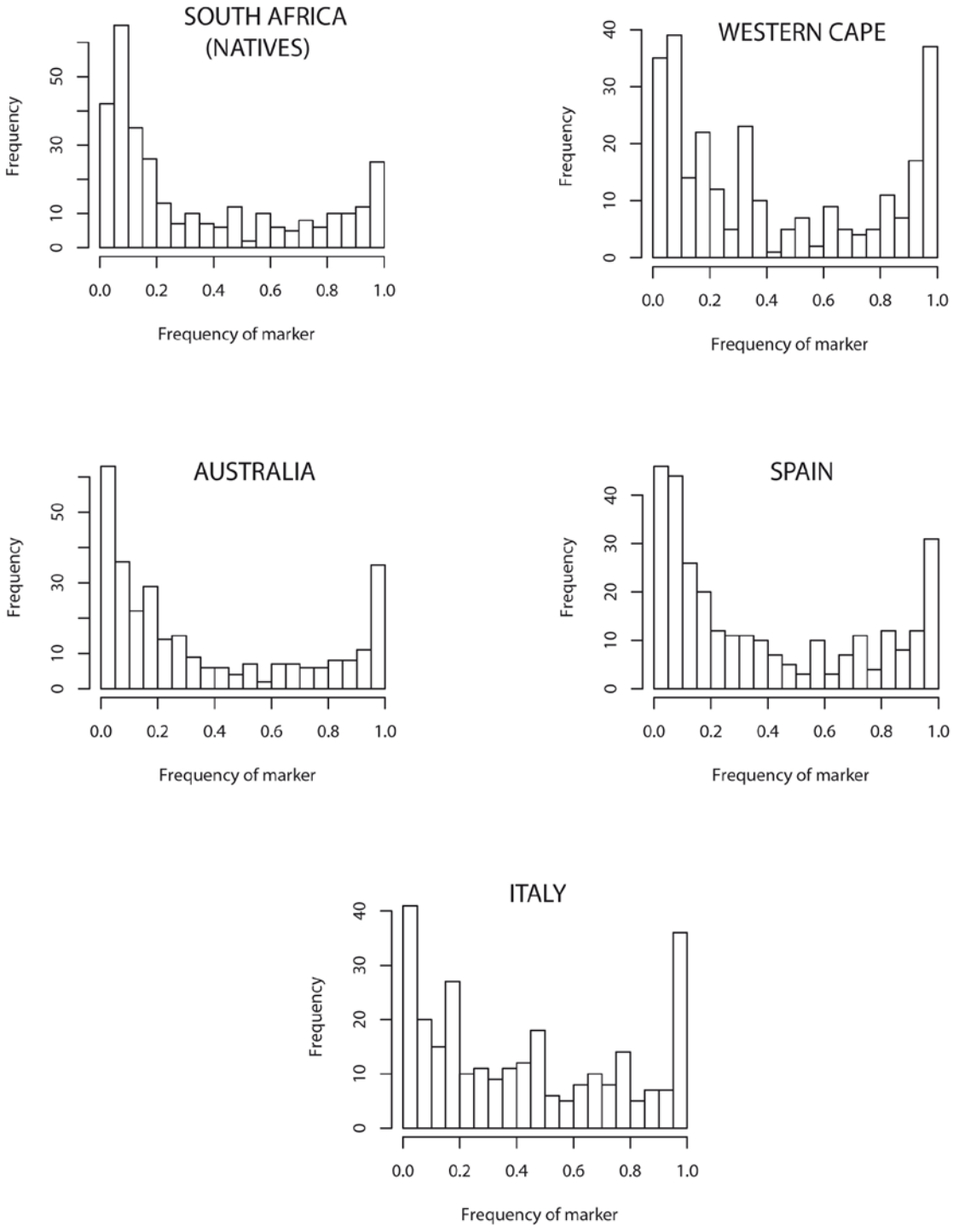
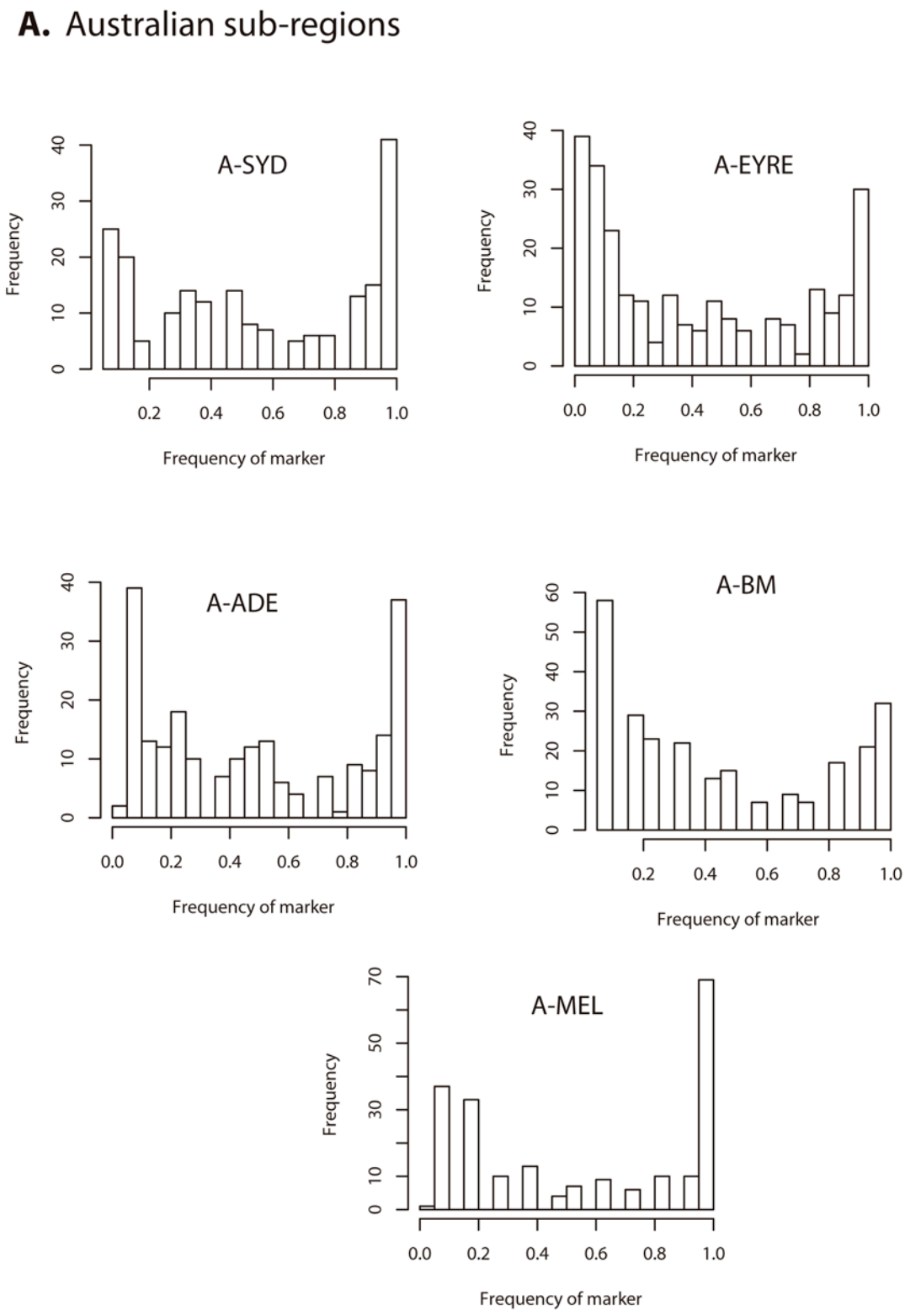


Figure S5. A, Marker frequency distribution for each of the five Australian sub-regions studied. B, Marker frequency distribution for each of the Spanish sub-regions studied. Only polymorphic markers are included. Australian sub-regions: A-SYD = Sydney area, A-EYRE = Eyre Peninsula area, A-ADE = Adelaide area, A-BM = Barker-Mallee area, A-MEL = Melbourne area; Spanish sub-regions: CAT-N= North Catalonia, CAT-S= South Catalonia.



Vilatersana R, Sanz M, Galian A, Castells E (2016) Biological Invasions
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Figure S5 (continuation)

B. Spanish sub-regions

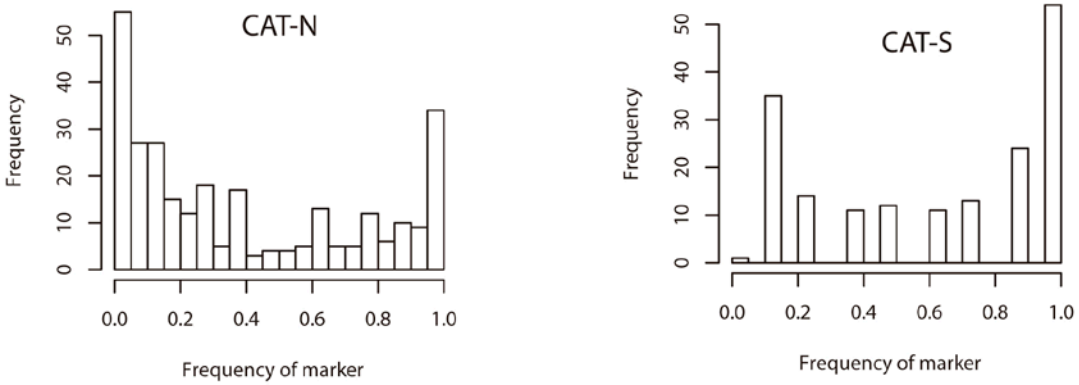

Figure S6. A, Total metric tons (Tn) of unwashed wool imported from Australia and South Africa to Spain from 1951 to 1986 B, Percentage of imported wool from Australia and South Africa in comparison to total amount imported (Estadística del comercio exterior de España 1951-1989)